

## Errata and Corrigenda

The publishers and the authors would like to make the following correction:

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Dariusz N., Fisher C.W., Cox R.P., Chuang, D.T., Structure of the gene encoding the entire mature E1 $\alpha$  subunit of human branched-chain  $\alpha$ -keto acid dehydrogenase complex (1991) FEBS Letters 284, 34–38

1 Figure 2 was mislabeled and two portions of the sequence were separated and in incorrect order

See below and next page for correct figure and legend

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Fig. 2 Nucleotide and deduced amino acid sequences of the exons of human E1 $\alpha$  gene. Exonic sequences are in capitals, and partial intronic sequences at exon/intron boundaries are in lower case. The approximate sizes of introns (except intron 1) are indicated. The highly conserved region (underlined) flanking the two phosphoserine (asterisk) residues is encoded by exon 8. The complete 3' end of the gene, which includes the polyadenylation signal (AATAAA) (underlined) terminates at base 1726. Nucleotide numbers are according to the human E1 $\alpha$  cDNA sequence [4]

2 On page 36, line 17 of the text in the left column, the size of exon 5 (106 bases) was an error. The correct size for exon 5 is 162 bases

3 Also on page 36, the second sentence in the right column should read

The upstream mitochondrial presequence from Gly-(−43) to Ser-(−10) in the E1 $\alpha$  cDNA is also absent in the genomic clone (Fig. 2)

Instead of

The upstream mitochondrial presequence from Gly-(−43) to Ala-(−10) in the E1 $\alpha$  cDNA is also absent in the genomic clone (Fig. 2)

|   |  |   |     |      |
|---|--|---|-----|------|
| -43   | -40  | -30   | -20 |      |
| GlyAlaIleAlaAlaAlaArgValTrpArgLeuAsnArgGlyLeuSerGlnAlaAlaLeuLeuLeuLeuArgGlnProGlyAla  |  |   |     |      |
| CGGGCGCATCGCTGCACGAGGGTCTGGCGGTAAACCGTGGTTTGAGCCAGGCTGCCCTCTCTCTCTCGGCLAGCCTGGGGCT    |  |   |     | 85   |
| -10   |  |   | 1   |      |
| ArgGlyLeuAlaArgSer  |  | HisProProArgGlnGlnGlnGlnPheSerSerLeuAspAspLysPro                |     |      |
| CGGGGACTGGCTAGATCT  |  | ctcttccccagCACCCCCCAGGCAGCAGCAGCAGTTTCATCTCTGGATGACAAGCCC       |     | 151  |
| 10  | 20   | 30  |     |      |
| GlnPheProGlyAlaSerAlaGluPheIleAspLysLeuGluPheIleGlnProAsnValIleSerGlyIleProIleTyrArg  |  |   |     |      |
| CAGTTCACGAGGCGCTCGGCGGAGTTTATAGATAAGTTGGAATTCATCCAGCCCAACGTCATCTCTGGAATCCCCATCTACCGC  |  |   |     | 235  |
| 40  | 50   |   |     |      |
| ValMetAspArgGlnGlyGlnIleIleAsnProSerGluAspProHis                                      |  |   |     |      |
| GTCATGGACCGGCAAGCCAGATCATCAACCCAGCGAGGACCCCAACGtggagggcgggctcccccaattccccgtccccca     |  |   |     | 283  |
| cgccccagggc   | /0 1 kb/   | ccaactgccccacgtctatctgtgctccaccgcagCTGCCGAAGGAGAAGGTGCTG        |     | 304  |
| 60  | 70   | 80  |     |      |
| LysLeuTyrLysSerMetThrLeuLeuAsnThrMetAspArgIleLeuTyrGluSerGlnArgGln                    |  |   |     |      |
| AAGCTCTACAAGAGCATGACATGCTTAACACCATGGACCGCATCTCTATGAGTCTCAGCGGCAGgtgctgg               |  | /3 1  |     | 370  |
|   | 90   | 100   |     |      |
| kb/   | GlyArgIlePhePheTyrMetThrAsnTyrGlyGluGluGlyThrHisValGlySerAla             |   |     |      |
|   | ccactccacccccagGGCCGATCTCTCTACATGACCAACTATGGTGAGGAGGGCACGCACGTCGGGAGTGCC |   |     | 430  |
|   | 110  |   |     |      |
| AlaAlaLeuAspAsnThrAspLeuValPheGlyGlnTyrArgGluAlaG                                     |  |   |     |      |
| GGCGCCCTGGACAACACGACCTGGTGTGTTGGCCAGTACCGGAGGCGAGgtacgtct                             | /5 0 kb/   | ctctctccccct  |     | 479  |
| 120   | 130  | 140   |     |      |
| lyValLeuMetTyrArgAspTyrProLeuGluLeuPheMetAlaGlnCysTyrGlyAsnIleSerAspLeuGlyLysGly      |  |   |     |      |
| cctagGTGTGCTGATGTATCGGACTACCCCTGGAACTATTTCATGCCCCAGTGTCTATGGCAACATCAGTGACTTGGGAAGGGG  |  |   |     | 559  |
| 150   | 160  | 170   |     |      |
| ArgGlnMetProValHisTyrGlyCysLysGluArgHisPheValThrIleSerSerProLeuAlaThrGlnIleProGlnA    |  |   |     |      |
| CGCCAGATGCTGTCCACTACGGCTGCAAACACGCCACTTCGTCTACTATCTCTCTCCACTGGCCACGCAGATCCCTCAGGgtg   |  |   |     | 641  |
|   | 180  |   |     |      |
| aggat   | /3 1 kb/   | tctcatccccctgcagCGGTGGGGCGGCGTACGCAGCCAAGCGGGCCAATGCCAACAGGGTCT |     | 668  |
| 190   | 200  | 210   |     |      |
| ValIleCysTyrPheGlyGluGlyAlaAlaSerGluGlyAspAlaHisAlaGlyPheAsnPheAlaAlaThrLeuGluCysPro  |  |   |     |      |
| GTCATCTGTTACTTCGGCGAGGGGGCAGCCAGTGAGGGGGACGCCCATGCGGGTTCAACTTCGCTGCCACACTTGAGTGCCCC   |  |   |     | 772  |
| 220   | 230  |   |     |      |
| IleIlePhePheCysArgAsnAsnGlyTyrAlaIleSerThrProThrSerGluGlnTyrArgGlyAspGlyIleA          |  |   |     |      |
| ATCATCTTCTTCTGCCGGAACAATGGCTACGCCATCTCCAGGCCACCTCTGAGCAGTATCGCGCGATGGCATTGgtatgggc    |  |   |     | 848  |
|   | 240  | 250   |     |      |
| /0 3 kb/  | laAlaArgGlyProGlyTyrGlyIleMetSerIleArgValAspGlyAsnAsp                    |   |     |      |
|   | tctgtgtccccacagCAGCACGAGGCCCGGGTATGGCATCATGTCAATCCGCGTGATGGTAATGAT       |   |     | 901  |
| 260   | 270  | 280   |     |      |
| ValPheAlaValTyrAsnAlaThrLysGluAlaArgArgAlaValAlaGluAsnGlnProPheLeuIleGluAlaMetThr     |  |   |     |      |
| GTGTTTGCCGTATACAAGCCACAAAGGAGGCCCCAGCGGGGCTGTGGCAGAGAACCAGCCCTTCTCATCGAGGCCATGACC     |  |   |     | 985  |
|   | 290  | 300   |     |      |
| TyrAr   | gileGlyHisHisSerThrSerAspAspSerSerAlaTyr                                 |   |     |      |
| TACAGgtgctgc  | /0 2 kb/   | cttgccccctgtgcagGATCGGGCACCACAGCACCAGTACGACAGCTTCAGCGTAC        |     | 1030 |
| *   | 310  | 320   |     |      |
| ArgSerValAspGluValAsnTyrTrpAspLysGlnAspHisProIleSerArgLeuArgHisTyrLeuLeuSerGlnGlyTrp  |  |   |     |      |
| CGCTCGGTGGATGAGGTCAATTACTGGGATAAACAGGACCACCCCATCTCCCGCTGCGGCACATCTGCTGAGCCAAGGCTGG    |  |   |     | 1114 |
| 330   | 340  |   |     |      |
| TrpAspGluGluGlnGluLysAlaTrpArgLysGlnSerArgArgLys                                      |  |   |     |      |
| TGGATGAGCAGCAGGAGAAGCCCTGGAGGAAGCAGTCCCGCAGGAAGgtgaggggt                              | /1 2 kb/   | ccccgtcccc  |     | 1162 |
|   | 350  | 360   | 370 |      |
| ValMetGluAlaPheGluGlnAlaGluArgLysProLysProAsnProAsnLeuLeuPheSerAspValTyrGlnGluMet     |  |   |     |      |
| acagGTGATGGAGGCCCTTGAGCAGGCCGAGCGGAAGCCCAACCCCAACCTGCTCTCTCAGACGTGTATCAGGAGATG        |  |   |     | 1243 |
|   | 380  | 390   |     |      |
| ProAlaGlnLeuArgLysGlnGlnGluSerLeuAlaArgHisLeuGlnThrTyrGlyGluHisTyrProLeuAspHisPheAsp  |  |   |     |      |
| CCCCCGAGCTCCGCAAGCAGCAGGAGTCTCTGGCCCGCCACCTGCAGACCTACGGGGAGCACTACCCACTGGATCACTTCGAT   |  |   |     | 1327 |
| 400   |  |   |     |      |
| Lys***  |  |   |     |      |
| AACTGAGACCTGCTCAGCCCAACCCCAACCCATCCTCAGCTACCCCGAGAGGTAGCCCCACTCTAAGGGGAGCAGGGGGACCTGA |  |   |     | 1411 |
| CAGCACACCACTGTCTTCCCGAGTCAGCTCCCTCTAAAATACCTCAGCGGGCAGGGCGGCTGCCACTCTTACCCCTGTCTCTCC  |  |   |     | 1495 |
| CGGCTCTTACATCTGTCAGGGGACAGCATCTGCAGCAGTTGCTGAGGCTCCGTCAGCCCCCTCTTACCTGTTGTTACAGTGCCT  |  |   |     | 1579 |
| TCTCCAGGGGCTGCGTGAGGGGACATTCAGGACTAGAACCCCTCTGGGCATGGGCTGGACATGGCAGGTCAGCCTGTGGAAC    |  |   |     | 1663 |
| TTGCGCAGGTGCGAGTGGCCAGCAGAGGTACCGAATAAACTGCATCTCTGCGCTGGCTCTCT                        |  |   |     | 1726 |